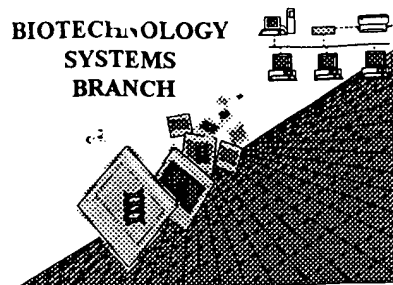


## **RAW SEQUENCE LISTING** **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/403,440  
Source: 1600 RUSH  
Date Processed by STIC: 2/10/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

## Raw Sequence Listing Error Summary

### ERROR DETECTED      SUGGESTED CORRECTION

SERIAL NUMBER: 09/403,440

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos      was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will  
     prevent "wrapping."
  
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers;  
     Numbering      use space characters, instead.
  
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please  
     ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules,  
     each n or Xaa can only represent a single residue. Please present the maximum number of each  
     residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"      sequences(s)     . Normally, PatentIn would automatically generate this section from the  
     previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
     the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for  
     Artificial or Unknown sequences.
  
- 7      Skipped Sequences      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
     (OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
     (i)      SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
     This sequence is intentionally skipped  
  
     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
     (NEW RULES)      <210> sequence id number  
     <400> sequence id number  
     000
  
- 9      Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing  
     (NEW RULES)      Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
     Response      scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
     is Artificial Sequence
  
- 11      Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
     Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
     "Unknown." Please explain source of genetic material in <220> to <223> section.  
     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"      resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
     listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1642

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/403,440

DATE: 07/10/2001  
TIME: 09:16:31

Input Set : A:\09403440.txt  
Output Set: N:\CRF3\07102001\I403440.raw

Does Not Comply  
Corrected Diskette Needed

1 <110> APPLICANT: Lane, David Philip  
W--> 2 <120> TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO  
W--> 3 INHIBITING THE INTERACTION OF p53 AND MDM2  
W--> 4 <130> FILE REFERENCE: MEWB25.001APC  
W--> 5 <140> CURRENT APPLICATION NUMBER: 09/403,440  
C--> 6 <141> CURRENT FILING DATE: 2000-01-19  
7 <150> PRIOR APPLICATION NUMBER: PCT/GB98/01144  
8 <151> PRIOR FILING DATE: 1998-04-20  
9 <150> PRIOR APPLICATION NUMBER: GB 9708092.3  
10 <151> PRIOR FILING DATE: 1997-04-22  
W--> 11 <160> NUMBER OF SEQ ID: 12  
12 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
14 <210> SEQ ID NO: 1  
15 <211> LENGTH: 5  
16 <212> TYPE: PRT  
17 <213> ORGANISM: Unknown  
W--> 18 <220> FEATURE:  
19 <223> OTHER INFORMATION: (Unknown) give source of genetic material - see  
20 <221> NAME/KEY: UNSURE item 11 on  
21 <222> LOCATION: 2,3 Error summary  
22 <223> OTHER INFORMATION: Xaa = any amino acid sheet  
W--> 23 <400> SEQUENCE: 1  
WOK 24 Phe Xaa Xaa Leu Trp  
25 1 5  
27 <210> SEQ ID NO: 2  
28 <211> LENGTH: 19  
29 <212> TYPE: PRT  
30 <213> ORGANISM: E. coli  
WOK 31 <400> SEQUENCE: 2  
32 Pro Pro Leu Ser Gln Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro  
33 1 5 10 15  
34 Glu Asn Gly  
36 <210> SEQ ID NO: 3  
37 <211> LENGTH: 19  
38 <212> TYPE: PRT  
39 <213> ORGANISM: E. coli  
WOK 40 <400> SEQUENCE: 3  
41 Pro Pro Leu Ser Met Pro Arg Phe Met Asp Tyr Trp Glu Gly Leu Asn  
42 1 5 10 15  
43 Glu Asn Gly  
45 <210> SEQ ID NO: 4  
46 <211> LENGTH: 5  
47 <212> TYPE: PRT  
48 <213> ORGANISM: Unknown  
W--> 49 <220> FEATURE:  
50 <223> OTHER INFORMATION: (Unknown) same error  
51 <221> NAME/KEY: UNSURE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/403,440

DATE: 07/10/2001

TIME: 09:16:31

Input Set : A:\09403440.txt

Output Set: N:\CRF3\07102001\I403440.raw

52 <222> LOCATION: 2,3,4  
 53 <223> OTHER INFORMATION: Xaa= any amino acid  
 W--> 54 <400> SEQUENCE: 4  
 W/C-> 55 Phe Xaa Xaa Xaa Trp  
 56 1 5  
 58 <210> SEQ ID NO: 5  
 59 <211> LENGTH: 57  
 60 <212> TYPE: DNA  
 61 <213> ORGANISM: Artificial Sequence  
 W--> 62 <220> FEATURE:  
 63 <223> OTHER INFORMATION: Synthetic peptide *This is not a peptide sequence*  
 W--> 64 <400> SEQUENCE: 5  
 65 gtccgcctct gagtcaggaa acattttcag acctatggaa actacttcct gaaaacg 57  
 67 <210> SEQ ID NO: 6  
 68 <211> LENGTH: 57  
 69 <212> TYPE: DNA  
 70 <213> ORGANISM: Artificial Sequence  
 W--> 71 <220> FEATURE:  
 72 <223> OTHER INFORMATION: Synthetic peptide  
 W--> 73 <400> SEQUENCE: 6  
 74 gaccgttttc aggaagtagt ttccataggt ctgaaaatgt ttcctgactc agaggcg 57  
 76 <210> SEQ ID NO: 7  
 77 <211> LENGTH: 57  
 78 <212> TYPE: DNA  
 79 <213> ORGANISM: Artificial Sequence  
 W--> 80 <220> FEATURE:  
 81 <223> OTHER INFORMATION: Synthetic peptide  
 W--> 82 <400> SEQUENCE: 7  
 83 gtccgcctct gagtatgcct cgttttatgg attattggga gggctctaata gaaaacg 57  
 85 <210> SEQ ID NO: 8  
 86 <211> LENGTH: 59  
 87 <212> TYPE: DNA  
 88 <213> ORGANISM: Artificial Sequence  
 W--> 89 <220> FEATURE:  
 90 <223> OTHER INFORMATION: Synthetic peptide  
 W--> 91 <400> SEQUENCE: 8  
 92 gaccgttttc attaagaccc tccaataat ccataaaaacg aggcatactc tcagaggcg 59  
 94 <210> SEQ ID NO: 9  
 95 <211> LENGTH: 35  
 96 <212> TYPE: DNA  
 97 <213> ORGANISM: Artificial Sequence  
 W--> 98 <220> FEATURE:  
 99 <223> OTHER INFORMATION: ~~OTHER INFORMATION:~~ Synthetic peptide *delete - do not use alphabetical headers*  
 W--> 100 <400> SEQUENCE: 9 *not a peptide sequence*  
 101 cgggatccac catgggcatg aaaattattc acctg 35  
 103 <210> SEQ ID NO: 10  
 104 <211> LENGTH: 29  
 105 <212> TYPE: DNA  
 106 <213> ORGANISM: Artificial Sequence

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/403,440

DATE: 07/10/2001  
TIME: 09:16:31

Input Set : A:\09403440.txt  
Output Set: N:\CRF3\07102001\I403440.raw

W--> 107 <220> FEATURE:  
108 <223> OTHER INFORMATION: (Synthetic peptide)  
W--> 109 <400> SEQUENCE: 10 29  
110 ctcgacgcta acctggccta gggaattcc  
112 <210> SEQ ID NO: 11  
113 <211> LENGTH: 26  
114 <212> TYPE: DNA  
115 <213> ORGANISM: Artificial Sequence  
W--> 116 <220> FEATURE:  
117 <223> OTHER INFORMATION: (Synthetic peptide)  
W--> 118 <400> SEQUENCE: 11 26  
119 gactctgggg atcgatatga ccgacc  
121 <210> SEQ ID NO: 12  
122 <211> LENGTH: 27  
123 <212> TYPE: DNA  
124 <213> ORGANISM: Artificial Sequence  
W--> 125 <220> FEATURE:  
126 <223> OTHER INFORMATION: (Synthetic peptide)  
W--> 127 <400> SEQUENCE: 12 27  
128 gagccaggag acagcctcag gcttatg

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/403,440

DATE: 07/10/2001

TIME: 09:16:32

Input Set : A:\09403440.txt

Output Set: N:\CRF3\07102001\I403440.raw

L:2 M:283 W: Missing Blank Line separator, <120> field identifier  
L:4 M:283 W: Missing Blank Line separator, <130> field identifier  
L:5 M:283 W: Missing Blank Line separator, <140> field identifier  
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:11 M:283 W: Missing Blank Line separator, <160> field identifier  
L:18 M:283 W: Missing Blank Line separator, <220> field identifier  
L:23 M:283 W: Missing Blank Line separator, <400> field identifier  
L:24 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:31 M:283 W: Missing Blank Line separator, <400> field identifier  
L:40 M:283 W: Missing Blank Line separator, <400> field identifier  
L:49 M:283 W: Missing Blank Line separator, <220> field identifier  
L:54 M:283 W: Missing Blank Line separator, <400> field identifier  
L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:62 M:283 W: Missing Blank Line separator, <220> field identifier  
L:64 M:283 W: Missing Blank Line separator, <400> field identifier  
L:71 M:283 W: Missing Blank Line separator, <220> field identifier  
L:73 M:283 W: Missing Blank Line separator, <400> field identifier  
L:80 M:283 W: Missing Blank Line separator, <220> field identifier  
L:82 M:283 W: Missing Blank Line separator, <400> field identifier  
L:89 M:283 W: Missing Blank Line separator, <220> field identifier  
L:91 M:283 W: Missing Blank Line separator, <400> field identifier  
L:98 M:283 W: Missing Blank Line separator, <220> field identifier  
L:100 M:283 W: Missing Blank Line separator, <400> field identifier  
L:107 M:283 W: Missing Blank Line separator, <220> field identifier  
L:109 M:283 W: Missing Blank Line separator, <400> field identifier  
L:116 M:283 W: Missing Blank Line separator, <220> field identifier  
L:118 M:283 W: Missing Blank Line separator, <400> field identifier  
L:125 M:283 W: Missing Blank Line separator, <220> field identifier  
L:127 M:283 W: Missing Blank Line separator, <400> field identifier